## Abstract of the Disclosure

A technique is described for determining the effectiveness of medical therapy and dosage formulations by analyzing dot spectrograms representative of quantized hybridization activity in biological samples, such as DNA, RNA or other protein biomolecular array samples, taken at different sampling times from a patient undergoing the treatment. The technique directly lends itself to disease progression analysis based on markers such as viral load. In accordance with the technique, a viral diffusion curve associated with a therapy of interest is generated and each dot spectrogram is then mapped to the viral diffusion curve using fractal filtering to yield a filtered viral diffusion curve for each sample. A degree of convergence between the filtered viral diffusion curves is determined. Then, a determination is made as to whether the therapy of interest has been effective by determining whether the degree of convergence increases from one sample to another, with an increase in the degree of convergence being representative of a lack of effectiveness of the therapy of interest. In a specific example described herein, the viral diffusion curve is generated by inputting parameters representative of viral load studies for the therapy of interest, generating a preliminary viral diffusion curve based upon the viral load studies and then calibrating a degree of directional causality in the preliminary viral diffusion curve to yield the viral diffusion curve. Each dot spectrogram is mapped to the viral diffusion curve using fractal filtering

by generating a partitioned iterated fractal system (IFS) model representative of the dot spectrogram, determining affine parameters for IFS model, and then mapping the dot spectrogram onto the viral diffusion curve using the IFS. Before the dot spectrogram is mapped to the viral diffusion curve, the dot spectrogram is interferometrically enhanced. After the mapping, any uncertainty in the filtered viral diffusion curve is compensated for using non-linear information filtering. A method is also described for determining the viral load within a biological sample by analyzing a dot spectrogram generated for the sample in connection with viral diffusion curves associated with a therapy of interest. Thus a technique is provided for detecting and tracking infections such as viral infections and establishing clinical endpoints, based on accurate biomolecular measurements of viral DNA or RNA in peripheral blood. The technique also provides a computational protocol for leveraging a clinical marker to establish and track therapy effectiveness based on quantification of amplified nucleic acid i.e., DNA and RNA assays. The technique can potentially amplify dynamic ranges over 100X or more over conventional assays. The technique enables point-of-care viral load detection biosensors to reliably predict the likelihood of disease progression and thereby allows the patient to make earlier and more effective decisions about treatment.